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OS Macadamia integrifolia.
ID R20181 standard; Protein; 666 AA.
AC W62829;
DE 27-OCT-1998 (first entry)
DE Macadamia integrifolia antimicrobial protein.
KW antimicrobial protein; infestation; control.
OS Macadamia integrifolia.
FH Key location/Qualifiers
FT Peptide 1..28
FT /note= "signal peptide"
FT Protein 29..666
FT /note= "mature protein"
PN WO9827805-A1.
PD 02-JUL-1998.
PF 22-DEC-1997; AU0874.
PR 20-DEC-1996; AU-004275.
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Goulter KC, Green JL, Mannens JM, Marcus JP;
DR WPI: 98-377279/32.
DR N-PSDB; V42310.
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT useful for controlling microbial infestations of plants or mammals
PS Claim 1; Page 34-36; 96pp; English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
CC Sequence 666 AA;
SQ
Query Match 95.9%; Score 520; DB 1; Length 666;
Best Local Similarity 95.7%; Pred. No. 1,42e-35;
Matches 66; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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DB 117 NRQDPQOQYEQCQKRCQRETEPRHMQCQRCERREKRRKQKRYEQREDEEKY 176
QY 76 NRQDPQOQYEQCQKRCQRETEPRHMQCQRCERREKRRKQKRYEQREDEEKY 135
DB 177 EERKKEEDN 185
QY 136 EERKKEGDN 144
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QY 136 EERKKEGDN 144
RESULT 4
ID W62831 standard; Protein; 525 AA.
AC W62831;
DE 27-OCT-1998 (first entry)
DE Theobroma cacao antimicrobial protein.
KW antimicrobial protein; infestation; control.
OS Theobroma cacao.
PN WO9827805-A1.
PD 02-JUL-1998.
PF 22-DEC-1997; AU0874.
PR 20-DEC-1996; AU-004275.
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Goulter KC, Green JL, Mannens JM, Marcus JP;
DR WPI: 98-377279/32.
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT useful for controlling microbial infestations of plants or mammals
PS Claim 1; Page 47-49; 96pp; English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
CC Sequence 525 AA;
SQ
Query Match 40.8%; Score 221; DB 1; Length 525;
Best Local Similarity 56.6%; Pred. No. 6.01e-10;
Matches 30; Conservative 9; Mismatches 11; Indels 3; Gaps 2;
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DB 35 ERDPQOQYEQCQKRCQRETEPRHMQCQRCERREKRRKQKRYEQREDEEKY 84
QY 78 QRPDPQOQYEQCQKRCQRETEPRHMQCQRCERREKRRKQKRYEQREDEEKY 130
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RESULT 5
ID R20181 standard; Protein; 566 AA.
AC R20181;
DE 16-APR-1992 (first entry)
DE Sequence encoded by 67 kD T. cacao protein cDNA.
KW Cocoa; flavour; vicillin; seed storage protein.
OS Theobroma cacao.
PN WO9119801-A.
PD 26-DEC-1991.
PF 07-JUN-1991; G00914.
PR 11-JUN-1990; GB-013016.
PA (MRSC) MARS UK LTD.
PI Spencer ME, Hodge R, Deakin EA, Ashton S;
DR WPI: 92-024418/03.
DR N-PSDB; Q20377.
PT Recombinant cocoa proteins - are responsible for flavour in cocoa
PT beans and produced in large quantities using yeast and bacterial
PT expression vectors.
PS Claim 4; Fig 2; 59pp; English.
CC The inventors claim a 67 kD and 31 kD T. cacao protein, and
CC fragments, and encoding DNAs. The 47 kD and 31 kD proteins are
CC derived from the 67 kD precursor. T. cacao protein cDNA was
CC detected in a cDNA library prepared from immature cocoa beans RNA
CC using a probe based on the AA sequence of a CNBR peptide common to
CC the 47 kD and 31 kD polypeptides. Homology searches revealed close
CC homologues between the 67 kD polypeptide and the vicilins, which are
CC seed storage proteins.
CC Sequence 566 AA;
SQ
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Query Match 94.5%; Score 512; DB 1; Length 666;
Best Local Similarity 94.2%; Pred. No. 7.11e-35;
Matches 65; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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DB 117 NRQDPQOQYEQCQKRCQRETEPRHMQCQRCERREKRRKQKRYEQREDEEKY 176
QY 76 NRQDPQOQYEQCQKRCQRETEPRHMQCQRCERREKRRKQKRYEQREDEEKY 135
DB 177 EERKKEEDN 185
QY 136 EERKKEGDN 144
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```
Query Match 40.8%; Score 221; DB 1; Length 566;
Best Local Similarity 56.6%; Pred. No. 6.01e-10;
Matches 30; Conservative 9; Mismatches 11; Indels 3; Gaps 2;
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DB 35 ERDPQOQYEQCQKRCQRETEPRHMQCQRCERREKRRKQKRYEQREDEEKY 84
QY 78 QRPDPQOQYEQCQKRCQRETEPRHMQCQRCERREKRRKQKRYEQREDEEKY 130
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RESULT 6

Query Match	22.98;	Score 124;	DB 1;	Length 444
Best Local Similarity	29.88;	Pred. No. 3.63e-02;		

CC animals

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SQ Sequence 593 AA:
Query Match 22.9%; Score 124; DB 1; Length 593;
Best Local Similarity 31.4%; Pred. No. 3.63e-02;
Matches 22; Conservative 16; Mismatches 28; Indels 4; Gaps 4;

Db 28 NHHHGGKSGCVCARCDPRPHQRP-R-CLEQC-REPEREKORRSRIHADRGEGSS 84
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 76 NKQRPQOYEQCKRCQRTETPRHMQICQRCERYEKERKQCKRYEQQREDEKY 135
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 85 EDERQEKER 94
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 136 E-ERMKEGDN 144

RESULT 10
ID W62841 standard; Protein; 28 AA.
AC W62841:
DT 27-OCT-1998 (first entry)
DE Stenocarpus sinuatus antimicrobial protein.
KW antimicrobial protein; infestation; control.
OS Stenocarpus sinuatus.
PN W09827805-A1.
PD 02-JUL-1998.
PF 22-DEC-1997; AU0874.
PR 20-DEC-1996; AU-004275.
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Goulter KC, Green JM, Manners JM, Marcus JP;
DR WPI: 98-377279/32.
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT useful for controlling microbial infestations of plants or mammals
PS Claim 1; Page 66; 96pp; English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
SQ Sequence 28 AA:

Query Match 20.3%; Score 110; DB 1; Length 28;
Best Local Similarity 50.0%; Pred. No. 4.17e-01;
Matches 13; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Db 2 DPIRQQLCOMRCQQQCKPRQOQC 27
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 80 DPQOYEQCKRCQRTETPRHMQIC 105

RESULT 11
ID W62836 standard; Protein; 33 AA.
AC W62836:
DT 27-OCT-1998 (first entry)
DE Zea mays antimicrobial protein.
KW antimicrobial protein; infestation; control.
OS Zea mays.
PN W09827805-A1.
PD 02-JUL-1998.
PF 22-DEC-1997; AU0874.
PR 20-DEC-1996; AU-004275.
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Goulter KC, Green JM, Manners JM, Marcus JP;
DR WPI: 98-377279/32.
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT useful for controlling microbial infestations of plants or mammals
PS Disclosure: Page 60; 96pp; English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
SQ Sequence 33 AA:

Query Match 20.1%; Score 109; DB 1; Length 33;
Best Local Similarity 44.4%; Pred. No. 4.96e-01;
Matches 12; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

Db 6 ECRROCLRHGQRPWETOECMRRCRR 32

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OY 87 QCKRCQRR-ETPRHMQICQRCERR 112
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 12
ID R21079 standard; Peptide; 35 AA.
AC R21079:
DT 09-APR-1992 (first entry)
DE Antimicrobial maize peptide, CMII.
KW Maize; CMII; corn; pathogen.
OS Zea mays.
PN EP-465009-A.
PD 08-JAN-1992.
PF 05-JUN-1991; 305064.
PR 05-JUN-1990; US-536127.
PA (PION-) PIONEER HI-BRED INT.
PI Duvick JP, Rood TA, Rao AG;
DR WPI: 92-010214/02.
PT Use of maize seed peptide CMII and DNA encoding it - for killing
PT or inhibiting plant pathogenic microorganisms.
PS Example 2; Page 5; 21pp; English.
CC The peptide (SEQ ID NO 1) was purified from public corn variety B73
CC and proprietary corn variety "MH18. It is basic and has a total
CC mol. wt. of 3900 daltons. The peptide sequence was used to design
CC probes which were used to screen a maize genomic or cDNA library.
CC The isolated CMII gene can be used to prepare an expression vector
CC for prodn. of recombinant CMII for use in controlling plant patho-
CC genic organisms.
CC See also Q20272 and 3.
SQ Sequence 35 AA:

Query Match 18.5%; Score 100; DB 1; Length 35;
Best Local Similarity 44.4%; Pred. No. 2.30e+00;
Matches 12; Conservative 6; Mismatches 8; Indels 1; Gaps 1;

Db 6 ECRROCLRHGQRPWETOECMRRCRR 32
OY 87 QCKRCQRR-ETPRHMQICQRCERR 112
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 13
ID R26941 standard; Protein; 316 AA.
AC R26941:
DT 08-FEB-1993 (first entry)
DE P.falciparum LSA-R-NR protein.
KW Malaria; hepatocyte; sporozoite; plasmid DG 536; T-cell epitope;
KW paludism; liver stage-specific antigen.
OS Plasmodium falciparum.
FH Key Location/Qualifiers
FT region 1..209
FT /label= repeat_region
FT /note= "contains 12 x 17mer repeats"
FT FT 210..316
FT /label= non-repeat_region

PN W09213884-A.
PD 20-AUG-1992.
PF 03-FEB-1992; F00104.
PR 05-FEB-1991; FR-001286.
PA (INSP) INST PASTEUR.
PI Drulhe P, Guerin-Marchand C, Guerinmarchand C;
DR WPI: 92-269985/36.
DR N-PSDB; Q28115.
PT Polyptide(s) derived from liver stage of Plasmodium falciparum
PT - for vaccination against, treatment of and diagnosis of malaria
PS Disclosure: Fig 1; 81pp; French.
CC A genomic DNA bank of P.falciparum EcoRI fragments prepared in
CC lambda gIII was used to transform E.coli. The expression library was
CC screened with human antisera against antigens of all stages of P.
CC falciparum. The library was rescreened with antibodies affinity-
CC purified on a clone which was able to recognise antibodies specific
CC to the hepatic phase. About 40 clones were detected which produced a
CC characteristic LSA epitope. The clone with the largest insert
CC (950 bases) encoded LSA-R-NR containing a 12-repeat region followed

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CC by a non-repeat region. Preferred antigenic polypeptides of the
CC invention are derived from the amino acid sequence of LSA-R-NR.
SQ Sequence 316 AA:

Query Match 18.5%; Score 100; DB 1; Length 316;
Best Local Similarity 36.8%; Pred. No. 2.30e+00;
Matches 25; Conservative 12; Mismatches 28; Indels 3; Gaps 3;

DB 161 RAKEKLOE-QOSDLEQERRAKEKLOEQSDLEQERR-AKEKLOEQORDLEQKADTKNL 218
OY 77 RQRDPQQQEQEQCKRQRRETERPRHMQIQQRCERREYKREKRRQKRYEQQREDEKXE 136
DB 219 ERKEHGD 226
OY 137 ERKKE-GD 143

RESULT 14
ID W90342 standard; protein; 409 AA.

AC W90342:
DT 24-MAY-1999 (first entry)
DE G. max truncated SBP2 protein.
KW SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
KW seed; carbohydrate content; soybean.
OS Glycine max.
PN W09853086-A1.

PD 26-NOV-1998.
PE 21-MAY-1998; U10465.
PR 22-MAY-1997; US-047568.
PA (UNIV) UNIV WASHINGTON STATE RES FOUND.
PI Chao WS, Grimes HD;

PT New modified plant sucrose binding proteins - used to develop
transgenic plants which can have enhanced or decreased sucrose
uptake activity in developing seeds
PS Claim 7; Page 39-40; 58pp; English.

CC This sequence represents a novel sucrose binding protein, SBP2 isolated
CC from Glycine max. This protein is used in a method resulting in the
CC production of a modified plant sucrose binding protein (SBP) which has a
CC modified amino acid sequence compared to a corresponding wild-type SBP.
CC and where expression of the modified SBP in a yeast assay system confers
CC enhanced sucrose uptake compared to the corresponding wild-type SBP.
CC The products of the invention can be used for producing transgenic plants
CC which have modified sucrose uptake activity, particularly in developing
CC seeds. Enhanced sucrose uptake activity in developing seeds may be
CC desirable where it is an advantage to increase the carbohydrate content
CC of the seed (e.g. where the seed is the primary plant material harvested,
CC such as soybean). In contrast, decreased sucrose uptake activity in
CC seeds might be desirable where the vegetative material of the plant is
CC harvested. The SBP regulatory regions confer specific or enhanced
CC expression in developing seeds and so may be used to express any
CC transgene in developing seeds.
SQ Sequence 409 AA:

Query Match 18.5%; Score 100; DB 1; Length 409;
Best Local Similarity 26.4%; Pred. No. 2.30e+00;
Matches 14; Conservative 18; Mismatches 18; Indels 3; Gaps 3;

DB 42 CKHCQQQQRQYTESDKRTCLQCCDSMKQERKQVEETREKEHEHQEHHEE 94
OY 88 CQKRCQR-RETETPRHMQIQQRCER-RYEKERR-KQKRYEQQREDEKXE 137

RESULT 15
ID W90341 standard; protein; 489 AA.

AC W90341:
DT 24-MAY-1999 (first entry)
DE G. max SBP2 protein.
KW SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
KW seed; carbohydrate content; soybean.
OS Glycine max.
PN W09853086-A1.
PD 26-NOV-1998.

PF 21-MAY-1998; U10465.
PR 22-MAY-1997; US-047568.
PA (UNIV) UNIV WASHINGTON STATE RES FOUND.
PI Chao WS, Grimes HD;

PT New modified plant sucrose binding proteins - used to develop
transgenic plants which can have enhanced or decreased sucrose
uptake activity in developing seeds
PS Claim 13b; Page 37-38; 58pp; English.

CC This sequence represents a novel sucrose binding protein, SBP2 isolated
CC from Glycine max. This protein is used in a method resulting in the
CC production of a modified plant sucrose binding protein (SBP) which has a
CC modified amino acid sequence compared to a corresponding wild-type SBP,
CC and where expression of the modified SBP in a yeast assay system confers
CC enhanced sucrose uptake compared to the corresponding wild-type SBP.
CC The products of the invention can be used for producing transgenic plants
CC which have modified sucrose uptake activity, particularly in developing
CC seeds. Enhanced sucrose uptake activity in developing seeds may be
CC desirable where it is an advantage to increase the carbohydrate content
CC of the seed (e.g. where the seed is the primary plant material harvested,
CC such as soybean). In contrast, decreased sucrose uptake activity in
CC seeds might be desirable where the vegetative material of the plant is
CC harvested. The SBP regulatory regions confer specific or enhanced
CC expression in developing seeds and so may be used to express any
CC transgene in developing seeds.
SQ Sequence 489 AA:

Query Match 18.5%; Score 100; DB 1; Length 489;
Best Local Similarity 26.4%; Pred. No. 2.30e+00;
Matches 14; Conservative 18; Mismatches 18; Indels 3; Gaps 3;

DB 42 CKHCQQQQRQYTESDKRTCLQCCDSMKQERKQVEETREKEHEHQEHHEE 94
OY 88 CQKRCQR-RETETPRHMQIQQRCER-RYEKERR-KQKRYEQQREDEKXE 137

Search completed: Sat May 13 10:33:45 2000
Job time : 8 secs.

